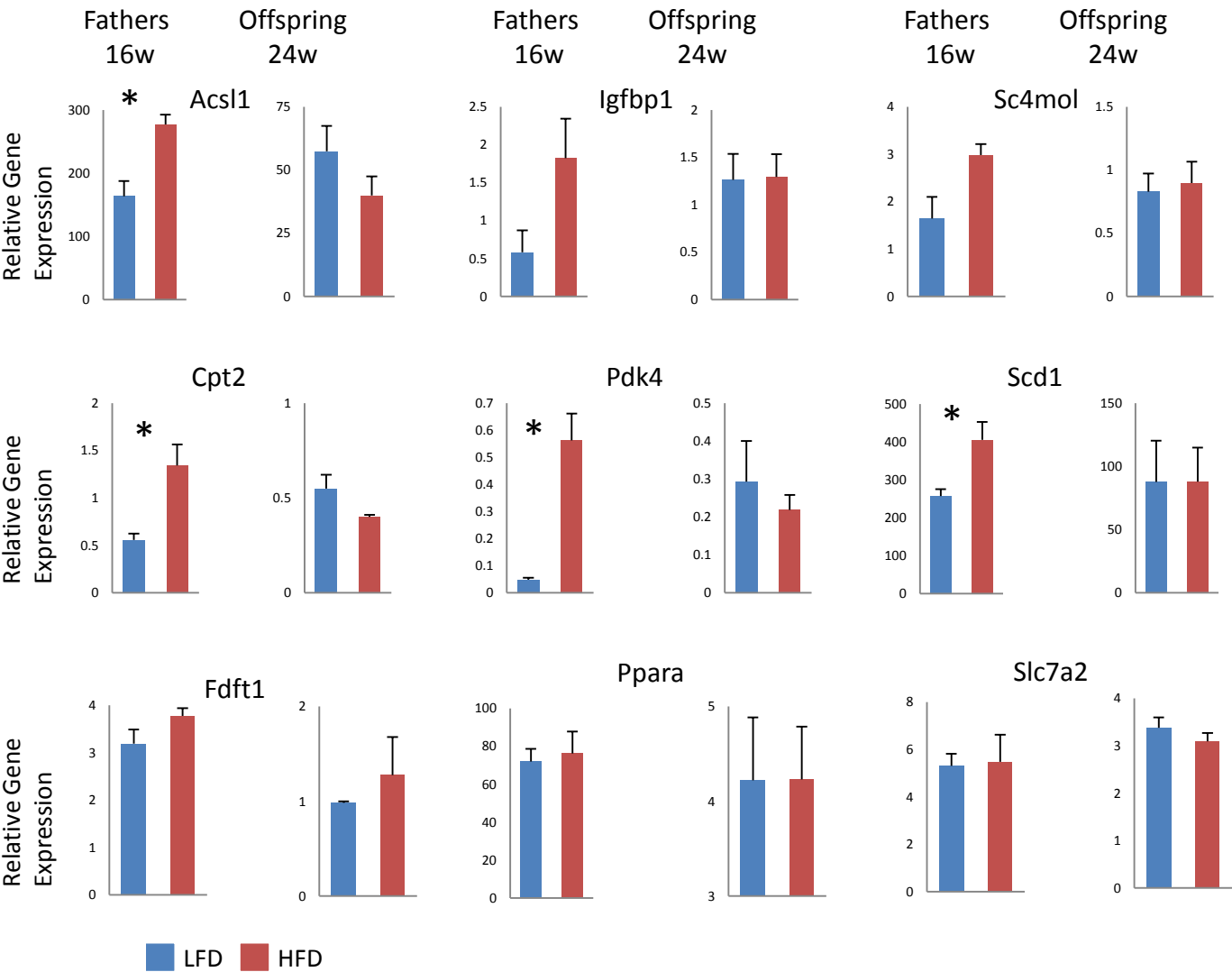
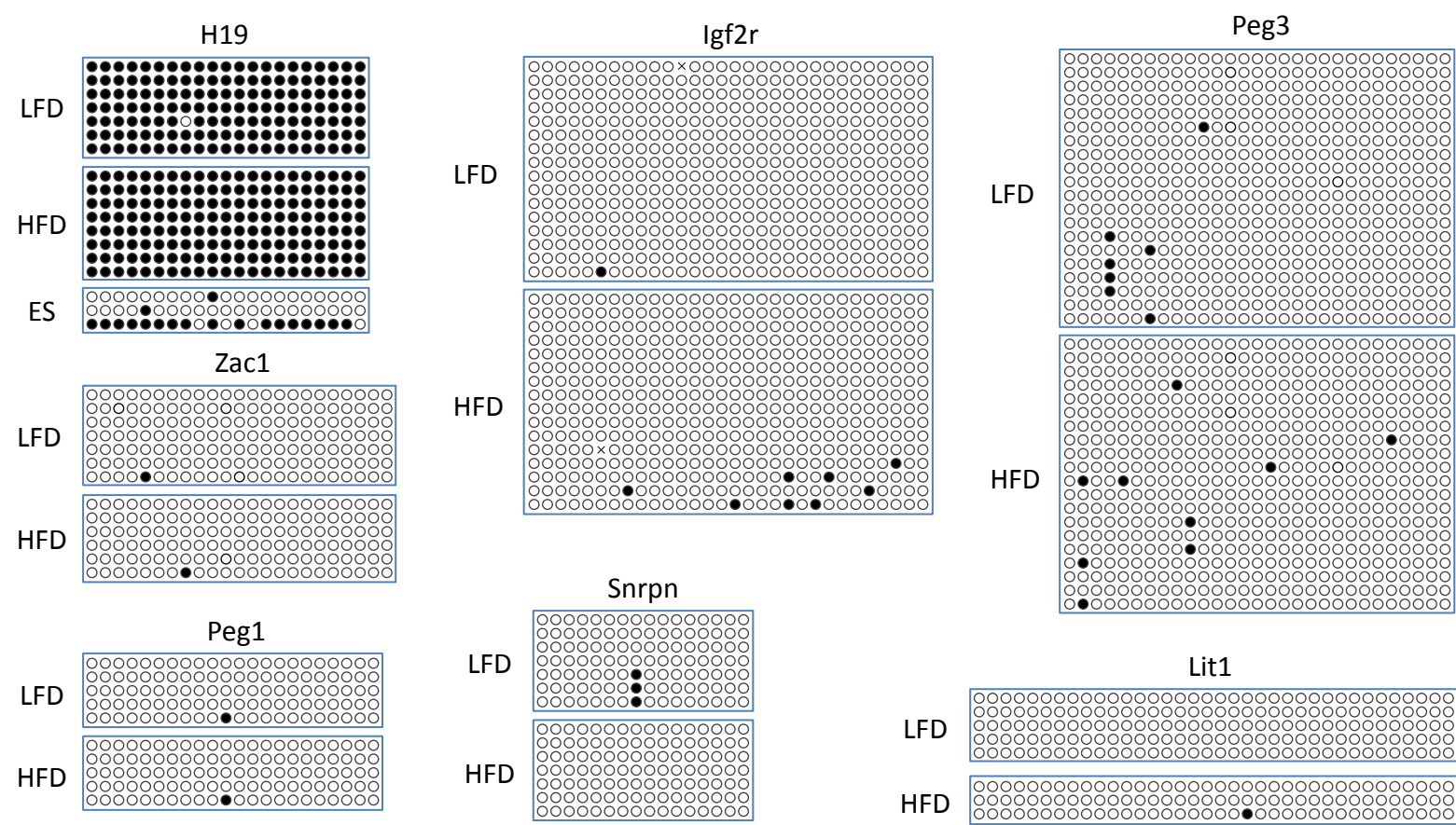


Supplement Fig 1



**Supplement Fig1: Gene expression in liver of male offspring and in liver of HFD fathers.** Real-time PCR analysis of mRNA expression derived from liver of HFD (red) and LFD (blue) father (left panel) or male offspring at 24 weeks of age (right panel). Each parental group summarizes the results (triplicates) of three animals as mean with standard error: HFD (n=3), LFD (n=3). The offspring represents the results in triplicates of four animals for each group: HFD (n=4), LFD (n=4).

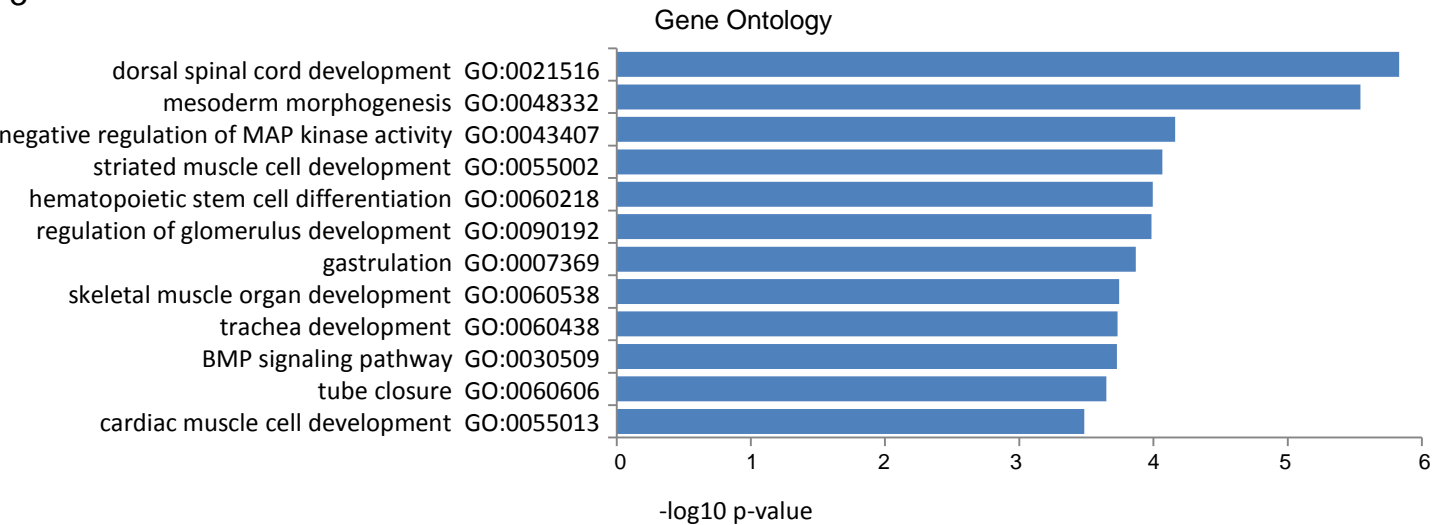
Supplement Fig 2



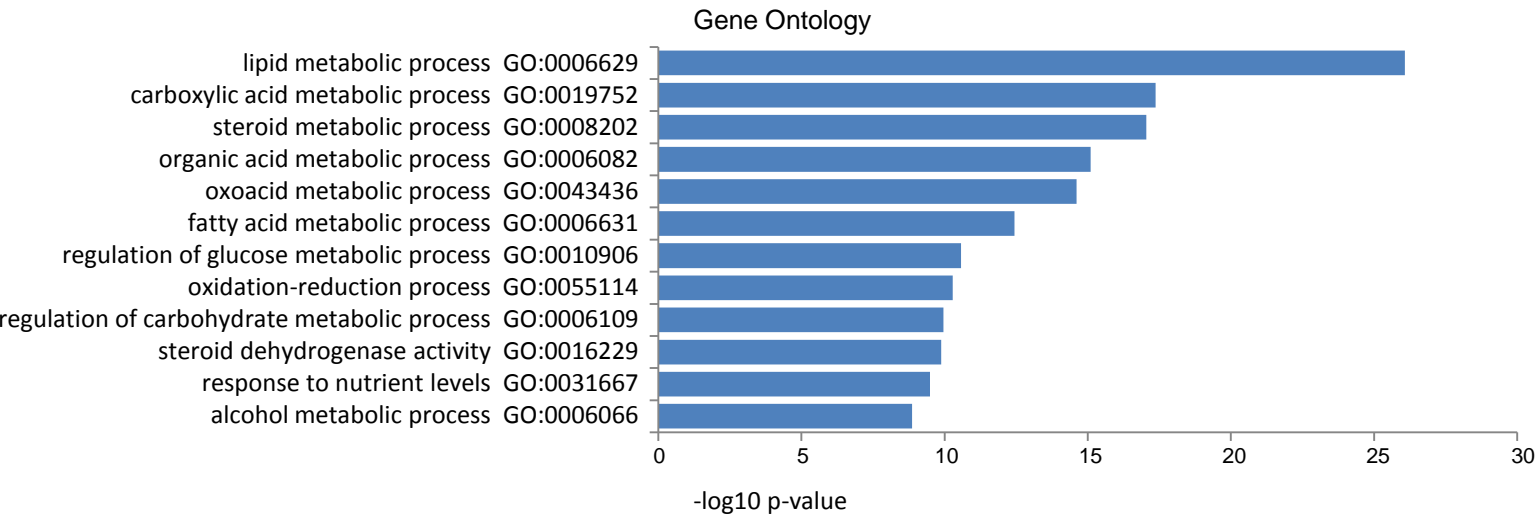
**Supplement Fig2: DNA methylation status of imprinted ICR in spermatozoa of HFD and LFD mice.** Genomic DNA was derived from spermatozoa of male mice fed for 10 weeks with HFD or LFD (Fig 1) and subjected to bisulfite sequencing analysis to determine CG methylation at the ICR of the indicated imprinted genes. The black filled circles represent CG methylation, while the white open circles indicate no methylation at specific CpG sites.

Supplement Fig 3

A

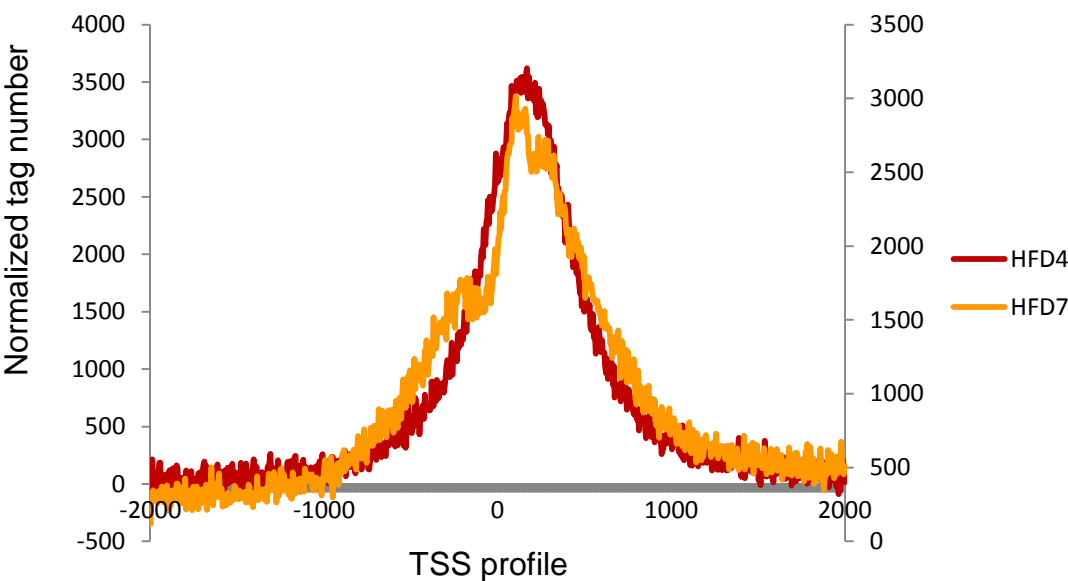


B



**Supplement Fig 3: Go term analysis for H3K4me1 enriched enhancers.** A. Go term analysis of top 10% of highly H3K4me1 enriched testis enhancer (n=945) in LFD5 over HFD4. B. Go term analysis of top 10% of highly H3K4me1 enriched liver enhancer (n=870) in LFD5 over HFD4.

Supplement Fig 4



**Supplement Fig 4: Peak localization at TSS.** Overlay of H3 enrichment profiles at TSS and 2kb of flanking sequences at protein coding genes (n=23,350) comparing HFD7 and HFD4 samples.